

## SEQUENCE LISTING

<110> Matuschek, Markus  
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Brakhage, Axel  
Achatz, Brigitte

<120> Method for producing carotenoids or their precursors using genetically modified organisms of the *Blakeslea* genus, carotenoids or their precursors produced by said method and use thereof

<130> 13311-00009-US

<150> PCT/EP2004/000099  
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<150> DE 103 00 649.4  
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24

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&lt;222&gt; (166)..(1155)

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120

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177

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225

Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys

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10

15

20

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273

Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp

25

30

35

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321

Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro

40

45

50

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369

Gly Leu Lys Asn Ala Tyr Lys Pro Pro Ser Asp Thr Lys Gly Ile

55

60

65

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417

Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His

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75

80

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Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp		
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Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser		
105 110 115		
ctg ctc gac atc gtc gta ttc ttt gtc ctg gag ttc ctg tac aca		561
Leu Leu Asp Ile Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr		
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Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu		
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tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac		705
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His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly		
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Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met		
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Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln		
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Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala		
230 235 240		
ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc		945
Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro		
245 250 255 260		
cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg		993
His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met		
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Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe		
280 285 290		
ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc		1089
Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro		
295 300 305		

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Phe Ala Pro Trp Trp Glu Ileu Pro Asn Cys Arg Arg Leu Ser Gly Arg	
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Gly Leu Val Pro Ala	
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35 40 45	

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp	
50 55 60	

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala	
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Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp

85

90

95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser  
 100 105 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu  
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly  
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Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val  
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Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys  
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His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp  
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met  
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr  
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Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe  
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly  
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Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser  
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Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp  
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Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His  
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Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser  
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Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser  
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Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro  
40 45 50  
cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc 368  
Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly  
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acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg 416  
Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro  
70 75 80  
aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc 464  
Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala  
85 90 95  
cag ctt ttg ggc gga agc agc cta ctg cac atc gct gca gtc ttc 512  
Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe  
100 105 110 115  
att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac 560  
Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp  
120 125 130

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Leu His Arg Lys His Trp Glu His Asn His Thr Gly Glu Val Gly			
165	170	175	
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Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe			
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Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu			
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245	250	255	
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Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp			
280	285	290	
gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc		1088	
Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys			
295	300	305	
cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga		1130	
Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala			
310	315	320	
cctggccct ccgctggta cccagcgtct gcacaagagt gtcatgctac agggtgctgc		1190	
ggccagttgc agcgcagtgc actctcagcc tgtatgggc taccgctgtg ccactgagca		1250	
ctggcatgc cactgagcac tggcgtgct actgagcaat gggcgtgcta ctgagcaatg		1310	
ggcgtgctac tgacaatggg cgtgctactg gggctggca tggagttga		1370	

tgcattcagt	agcgggtggcc	aacgtcatgt	ggatggtgga	agtgcgtgagg	ggtttaggca	1430
gccggcattt	gagagggcta	agttataaaat	cgcacatgc	tcatgcgcac	atatctgcac	1490
acagccaggg	aaatcccttc	gagagtgatt	atgggacact	tgtattggtt	tcgtgctatt	1550
gttttattca	gcagcagtac	ttagtgaggg	tgagagcagg	gtggtgagag	tggagtgagt	1610
gagtatgaac	ctggtcagcg	aggtgaacag	cctgtaatga	atgactctgt	ct	1662

<210> 14  
 <211> 320  
 <212> PRT  
 <213> Haematococcus pluvialis  
  
 <400> 14

Met	His	Val	Ala	Ser	Ala	Leu	Met	Val	Glu	Gln	Lys	Gly	Ser	Glu	Ala	
1					5				10				15			

Ala	Ala	Ser	Ser	Pro	Asp	Val	Leu	Arg	Ala	Trp	Ala	Thr	Gln	Tyr	His
						20		25				30			

Met	Pro	Ser	Glu	Ser	Ser	Asp	Ala	Ala	Arg	Pro	Ala	Leu	Lys	His	Ala
						35		40				45			

Tyr	Lys	Pro	Pro	Ala	Ser	Asp	Ala	Lys	Gly	Ile	Thr	Met	Ala	Leu	Thr
	50						55			60					

Ile	Ile	Gly	Thr	Trp	Thr	Ala	Val	Phe	Leu	His	Ala	Ile	Phe	Gln	Ile
	65				70				75			80			

Arg	Leu	Pro	Thr	Ser	Met	Asp	Gln	Leu	His	Trp	Leu	Pro	Val	Ser	Glu
					85			90				95			

Ala	Thr	Ala	Gln	Leu	Leu	Gly	Gly	Ser	Ser	Ser	Leu	Leu	His	Ile	Ala
								100			105			110	

Ala	Val	Phe	Ile	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr
					115			120			125				

Thr	His	Asp	Ala	Met	His	Gly	Thr	Ile	Ala	Leu	Arg	His	Arg	Gln	Leu
					130			135			140				

Asn	Asp	Leu	Leu	Gly	Asn	Ile	Cys	Ile	Ser	Leu	Tyr	Ala	Trp	Phe	Asp
					145			150			155			160	

Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly  
 165 170 175

Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val  
 180 185 190

Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe  
 195 200 205

Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro  
 210 215 220

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala  
 225 230 235 240

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro  
 245 250 255

Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr  
 260 265 270

Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp  
 275 280 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu  
 290 295 300

Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala  
 305 310 315 320

<210> 15  
 <211> 729  
 <212> DNA  
 <213> Agrobacterium aurantiacum

<220>  
 <221> CDS  
 <222> (1) .. (729)

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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat		96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His		
20 25 30		
gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca		144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala		
35 40 45		
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg		192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala		
50 55 60		
cat gac gcg atg cac ggg tcg gtg ccg ggg cgt ccg cgc gcc aat		240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn		
65 70 75 80		
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg		288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp		
85 90 95		
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc		336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr		
100 105 110		
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc		384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala		
115 120 125		
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc		432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro		
130 135 140		
gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac		480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr		
145 150 155 160		
gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc		528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe		
165 170 175		
gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg		576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro		
180 185 190		
gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg		624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu		
195 200 205		
ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac		672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His		
210 215 220		
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac		720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp		
225 230 235 240		
acc gca tga		729

Thr Ala

<210> 16  
 <211> 242  
 <212> PRT  
 <213> Agrobacterium aurantiacum  
 <400> 16

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

Ile Val Ser Gly Gly Ile Ala Ala Trp Leu Ala Leu His Val His  
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala  
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr  
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala  
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe  
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro

180

185

190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu  
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp  
 225 230 235 240

Thr Ala

<210> 17  
 <211> 1631  
 <212> DNA  
 <213> Alcaligenes sp.

<220>  
 <221> CDS  
 <222> (99)..(827)

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 ccggtctagg ctgtcgccct acgcagcagg agtttcgg atg tcc gga cg aag cct 116  
 Met Ser Gly Arg Lys Pro  
 1 5

ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164  
 Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile  
 10 15 20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212  
 Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp  
 25 30 35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260  
 Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr  
 40 45 50

tgg ctg tcg gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg 308  
 Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly  
 55 60 65 70

tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg 356  
 Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu  
 75 80 85

gcg ctg tgg ctc tat gcg ggg ttc tcg tgg ccc aag ctg atc gcc aag 404

Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys			
90	95	100	
cac atg acg cat cac cg <sup>g</sup> cac gcc ggc acc gac aac gat ccc gat ttc			452
His Met Thr His His Arg His Ala Gly Thr Asp Asn Asp Pro Asp Phe			
105	110	115	
ggt cac gga ggg ccc gtg cgc tgg tac ggc agc ttc gtc tcc acc tat			500
Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr			
120	125	130	
ttc ggc tgg cga gag gga ctg ctg cta ccg gtg atc gtc acc acc tat			548
Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro Val Ile Val Thr Thr Tyr			
135	140	145	150
gc <sup>g</sup> ctg atc ctg ggc gat cgc tgg atg tat gtc atc ttc tgg ccg gtc			596
Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr Val Ile Phe Trp Pro Val			
155	160	165	
ccg gcc gtt ctg gc <sup>g</sup> tcg atc cag att ttc gtc ttc gga act tgg ctg			644
Pro Ala Val Leu Ala Ser Ile Gln Ile Phe Val Phe Gly Thr Trp Leu			
170	175	180	
ccc cac cgc cc <sup>g</sup> gga cat gac gat ttt ccc gac ccg cac aac gc <sup>g</sup> agg			692
Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg			
185	190	195	
tcg acc ggc atc ggc gac cc <sup>g</sup> ttg tca cta ctg acc tgc ttc cat ttc			740
Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu Leu Thr Cys Phe His Phe			
200	205	210	
ggc ggc tat cac cac gaa cat cac ctg cat ccg cat gtg ccg tgg tgg			788
Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp			
215	220	225	230
cg <sup>g</sup> ctg cct cgt aca cgc aag acc gga gc <sup>g</sup> ccg gca tga cgcaattcct			837
Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly Arg Ala			
235	240		
cattgtcg <sup>t</sup> g gcgacagtcc tcgtgatgga gctgaccg <sup>t</sup> cc tattccgtcc accgctggat			897
tatgcacggc cccctaggct ggggctggca caagtccat cacgaagagc acgaccacgc			957
gttggagaag aacgacctct acggcgtcgt cttcgcggtg ctggcgacga tcctcttcac			1017
cgtggcgcc tattgg <sup>t</sup> ggc cggtgctgtg gtggatcgcc ctgggcatga cggtctatgg			1077
gtt <sup>t</sup> gatctat ttcatcctgc acgacgggct t <sup>t</sup> gtgcatcaa cgctggccgt ttcggtatat			1137
tccgcggcg <sup>t</sup> ggctatttcc gcaggctcta ccaagctcat cgcc <sup>t</sup> gcacc acgcgg <sup>t</sup> cg <sup>t</sup> a			1197
ggggcg <sup>t</sup> ggac cactgcgtca gcttcggctt catctatgcc ccacccgtgg acaagctgaa			1257
gcaggatctg aagcggtcgg gtgtcctgcg cccccaggac gagcgtccgt cgtatctct			1317
gatcccggcg <sup>t</sup> tggccgc <sup>t</sup> atg aaatccgacg tgctgctggc aggggcccggc cttgccaacg			1377

gactgatcg	gctggcgatc	cgcaaggcgc	ggcccac	tcgcgtgctg	ctgctggacc	1437
gtgcggcgg	cgcctcgac	ggcataactt	ggcctgcca	cgacaccgat	ttggcgccgc	1497
actggctgg	ccgcctgaag	ccgatcaggc	gtggcgactg	gcccgtcag	gaggtgcgg	1557
tcccagacca	ttcgcgaagg	ctccggccg	gatatggctc	gatgcacggg	cggggctga	1617
tgctgcgg	gacc					1631

<210> 18  
 <211> 242  
 <212> PRT  
 <213> Alcaligenes sp.

<400> 18

Met	Ser	Gly	Arg	Lys	Pro	Gly	Thr	Thr	Gly	Asp	Thr	Ile	Val	Asn	Leu
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Gly	Leu	Thr	Ala	Ala	Ile	Leu	Leu	Cys	Trp	Leu	Val	Leu	His	Ala	Phe
					20			25				30			

Thr	Leu	Trp	Leu	Leu	Asp	Ala	Ala	Ala	His	Pro	Leu	Leu	Ala	Val	Leu
					35			40			45				

Cys	Leu	Ala	Gly	Leu	Thr	Trp	Leu	Ser	Val	Gly	Leu	Phe	Ile	Ile	Ala
					50			55		60					

His	Asp	Ala	Met	His	Gly	Ser	Val	Val	Pro	Gly	Arg	Pro	Arg	Ala	Asn
65					70			75			80				

Ala	Ala	Ile	Gly	Gln	Leu	Ala	Leu	Trp	Leu	Tyr	Ala	Gly	Phe	Ser	Trp
					85			90			95				

Pro	Lys	Leu	Ile	Ala	Lys	His	Met	Thr	His	His	Arg	His	Ala	Gly	Thr
							100		105		110				

Asp	Asn	Asp	Pro	Asp	Phe	Gly	His	Gly	Gly	Pro	Val	Arg	Trp	Tyr	Gly
							115		120		125				

Ser	Phe	Val	Ser	Thr	Tyr	Phe	Gly	Trp	Arg	Glu	Gly	Leu	Leu	Leu	Pro
							130		135		140				

Val	Ile	Val	Thr	Thr	Tyr	Ala	Leu	Ile	Leu	Gly	Asp	Arg	Trp	Met	Tyr
						145		150		155		160			

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe  
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro  
 180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu  
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly  
 225 230 235 240

Arg Ala

<210> 19  
 <211> 729  
 <212> DNA  
 <213> Paracoccus marcusii

<220>  
 <221> CDS  
 <222> (1)..(729)

<400> 19  
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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96  
 Ile Val Ser Gly Gly Ile Ala Ala Trp Leu Ala Leu His Val His  
 20 25 30

gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144  
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala  
 35 40 45

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192  
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60

cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240  
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	
gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Leu Gly Asp Arg Trp Met Tyr	
145 150 155 160	
gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
180 185 190	
gac cgc cat aat gcg ccg tcg tcg ccg atc agc gac cct gtg tcg ctg	624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	
195 200 205	
ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac	672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His	
210 215 220	
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac	720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp	
225 230 235 240	
acc gca tga	729
Thr Ala	

<210> 20  
 <211> 242  
 <212> PRT  
 <213> Paracoccus marcusii

<400> 20

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

Ile Val Ser Gly Gly Ile Ala Ala Trp Leu Ala Leu His Val His

20

25

30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala  
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr  
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala  
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe  
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro  
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu  
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp  
 225 230 235 240

Thr Ala

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<210> 21
<211> 1629
<212> DNA
<213> Synechocystis sp.
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<221> CDS  
<222> (1) .. (1629)

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Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu				
1 5 10 15				
gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta				96
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu				
20 25 30				
gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg				144
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met				
35 40 45				
ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac				192
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His				
50 55 60				
gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag				240
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln				
65 70 75 80				
tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg				288
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly				
85 90 95				
ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt				336
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys				
100 105 110				
gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa				384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln				
115 120 125				
ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt				432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe				
130 135 140				
aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg				480
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp				
145 150 155 160				
gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg				528
Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala				

165	170	175	
ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn 180	185	190	576
gaa tgg ttc gac agc gaa cg <sup>g</sup> gtt aaa gct cct tta gct aga cta tgt Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys 195	200	205	624
tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met 210	215	220	672
atg atg gtg gcc atg cg <sup>g</sup> cat ttg gag gga att gcc aga cca aaa gga Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly 225	230	235	720
gcc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln 245	250	255	768
ggg gga aaa atc ctc act gac caa acc gtc aaa cg <sup>g</sup> gta ttg gtg gaa Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu 260	265	270	816
aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cg <sup>g</sup> Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg 275	280	285	864
gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu 290	295	300	912
caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly 305	310	315	960
gaa cga ctg gaa cg <sup>g</sup> cgc act gtg aac aat aac gaa gcc att tta aaa Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys 325	330	335	1008
atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly 340	345	350	1056
ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His 355	360	365	1104
gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala 370	375	380	1152
aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg			1200

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met				
385	390	395	400	
gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac				1248
Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr				
405		410	415	
cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc				1296
Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr				
420	425	430		
gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg				1344
Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr				
435	440	445		
gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa				1392
Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu				
450	455	460		
agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc				1440
Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val				
465	470	475	480	
tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta				1488
Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu				
485	490	495		
ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca				1536
Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr				
500	505	510		
ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga				1584
Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg				
515	520	525		
aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa				1629
Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp				
530	535	540		
<210> 22				
<211> 542				
<212> PRT				
<213> Synechocystis sp.				
<400> 22				
Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu				
1	5	10	15	
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu				
20	25	30		
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met				

35

40

45

Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His  
 50 55 60

Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln  
 65 70 75 80

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly  
 85 90 95

Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys  
 100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln  
 115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe  
 130 135 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp  
 145 150 155 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala  
 165 170 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn  
 180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys  
 195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met  
 210 215 220

Met Met Val Ala Met Arg His-Leu Glu Gly Ile Ala Arg Pro Lys Gly  
 225 230 235 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln  
 245 250 255

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu

260

265

270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg  
275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu  
290 295 300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly  
305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys  
325 330 335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly  
340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His  
355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala  
370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met  
385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr  
405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr  
420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr  
435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu  
450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val  
465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu  
485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr  
 500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg  
515 520 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp  
530 535 540

<210> 23  
<211> 776  
<212> DNA  
<213> *Bradyrhizobium* sp.

<220>  
<221> CDS  
<222> (1) .. (774)

<400> 23  
atg cat gca gca acc gcc aag gct act gag ttc ggg gcc tct cgg cgc 48  
Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg  
1 5 10 15

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gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc 96
Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
20          25          30

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atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg 144  
 Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro  
 35 40 45

ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192  
 Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln  
 50 55 60

acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac 240  
 Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His  
 65 70 75 80

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ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag 288
Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
85          90          95
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ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc 336  
 Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val  
 100 105 110

gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat 384  
 Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp  
 115 120 125

ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt	432
Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe	
130 135 140	
ttc ctg cac tat ttc ggc tgg aag cag gtc qcg atc atc gca gcc gtc	480
Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val	
145 150 155 160	
tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg	528
Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu	
165 170 175	
ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc	576
Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr	
180 185 190	
ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat	624
Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp	
195 200 205	
cgc cac aac gcg cggt acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg	672
Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu	
210 215 220	
acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat	720
Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp	
225 230 235 240	
gcg ccg tgg tgg cggt ctg ccg gag atc aag cggt ccg gcc ctg gaa agg	768
Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg	
245 250 255	
cgt gac ta	776
Arg Asp	

<210> 24  
 <211> 258  
 <212> PRT  
 <213> *Bradyrhizobium* sp.

<400> 24

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg  
 1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile  
 20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro  
 35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln

50

55

60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His  
 65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln  
 85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val  
 100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp  
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe  
 130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val  
 145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu  
 165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr  
 180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp  
 195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu  
 210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp  
 225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg  
 245 250 255

Arg Asp

<210> 25

<211> 777

<212> DNA  
<213> Nostoc sp.

<220>  
<221> CDS  
<222> (1) .. (777)

<400> 25  
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 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu  
 1 5 10 15  
  
 ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96  
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe  
 20 25 30  
  
 att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta 144  
 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu  
 35 40 45  
  
 ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc 192  
 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala  
 50 55 60  
  
 atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat 240  
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 65 70 75 80  
  
 gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat 288  
 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn  
 85 90 95  
  
 ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa 336  
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys  
 100 105 110  
  
 gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat 384  
 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp  
 115 120 125  
  
 tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg 432  
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp  
 130 135 140  
  
 tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga 480  
 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly  
 145 150 155 160  
  
 tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa 528  
 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu  
 165 170 175  
  
 aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta 576  
 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val  
 180 185 190

caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt	624
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly	
195 200 205	
ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt	672
Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe	
210 215 220	
tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac	720
Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His	
225 230 235 240	
gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata	768
Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile	
245 250 255	
tct tta taa	777
Ser Leu	

<210> 26  
 <211> 258  
 <212> PRT  
 <213> Nostoc sp.

<400> 26

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu	
1 5 10 15	

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe	
20 25 30	

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu	
35 40 45	

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala	
50 55 60	

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His	
65 70 75 80	

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn	
85 90 95	

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys	
100 105 110	

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp

115

120

125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp

130

135

140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly  
145 150 155 160Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu  
165 170 175Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val  
180 185 190Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly  
195 200 205Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe  
210 215 220Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His  
225 230 235 240Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile  
245 250 255

Ser Leu

<210> 27  
 <211> 789  
 <212> DNA  
 <213> Nostoc punctiforme

<220>  
 <221> CDS  
 <222> (1)...(789)

<400> 27  
 ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa 48  
 Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln  
 1 5 10 15

tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta 96  
 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val

20	25	30	
att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn 35 40 45			144
tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln 50 55 60			192
atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His 65 70 75 80			240
ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser 85 90 95			288
cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys 100 105 110			336
aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat Asn His Cys Leu His Arg His Pro Ala Ser Glu Val Asp Pro Asp 115 120 125			384
ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe 130 135 140			432
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu 145 150 155 160			480
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile 165 170 175			528
tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr 180 185 190			576
ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr 195 200 205			624
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile 210 215 220			672
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His 225 230 235 240			720
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn 245 250 255			768

aat tca gta acc aat tcg taa  
 Asn Ser Val Thr Asn Ser  
 260

789

<210> 28  
 <211> 262  
 <212> PRT  
 <213> Nostoc punctiforme

<400> 28

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln  
 1 5 10 15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val  
 20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn  
 35 40 45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln  
 50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His  
 65 70 75 80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser  
 85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys  
 100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp  
 115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe  
 130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu  
 145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile  
 165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr  
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr  
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile  
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn  
 245 250 255

Asn Ser Val Thr Asn Ser  
 260

<210> 29  
 <211> 762  
 <212> DNA  
 <213> Nostoc punctiforme

<220>  
 <221> CDS  
 <222> (1)..(762)

<400> 29  
 gtg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca 48  
 Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro  
 1 5 10 15

gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96  
 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val  
 20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144  
 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp  
 35 40 45

atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa 192  
 Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60

aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240  
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 65 70 75 80

ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288  
 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr

85	90	95	
ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys 100	105	110	336
aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat Lys His Trp Leu His His Asn Pro Ala Ser Ser Ile Asp Pro Asp 115	120	125	384
ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe 130	135	140	432
atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile 145	150	155	480
tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr 165	170	175	528
tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr 180	185	190	576
ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln 195	200	205	624
cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile 210	215	220	672
acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His 225	230	235	720
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<212> PRT  
<213> Nostoc punctiforme

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20

25

30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp  
 35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110

Lys His Trp Leu His His Asn Pro Ala Ser Ser Ile Asp Pro Asp  
 115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
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Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
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ggc cca cct cct cat ctc cat cggt tca ttt gct gct acc acg atg ctg		95
Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu		
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tcg aag ctg cag tca atc agc gtc aag gcc cgc gtc gaa cta gcc		143
Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala		
35             40                 45		
cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg		191
Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser		
50             55                 60		
tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga		239
Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly		
65             70                 75		
acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca		287
Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala		
80             85                 90                 95		
ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa		335
Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys		
100            105                 110		
cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc		383
Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ile Ala Ala Ser Ile Gly		
115            120                 125		
gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac		431
Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His		
130            135                 140		
atg acc gtg ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc		479
Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu		
145            150                 155		
ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat		527
Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr		
160            165                 170                 175		

gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His 180 185 190	575
aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu 195 200 205	623
ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly 210 215 220	671
ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu 225 230 235	719
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 35 40 45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu  
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Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr  
 65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu  
 85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg  
 100 105 110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ser Ile Gly Val  
 115 120 125

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met  
 130 135 140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu  
 145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala  
 165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys  
 180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe  
 195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe  
 210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly  
 225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val  
 245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys  
 260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly  
 275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro  
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Lys Arg

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atg gaa gtg att gct gca ctg gca cac aaa tac atc atg cac ggc tgg 96  
 Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp  
 20 25 30

ggt tgg gga tgg cat ctt tca cat cat gaa ccg cgt aaa ggt gcg ttt	144
Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe	
35 40 45	
gaa gtt aac gat ctt tat gcc gtg gtt ttt gct gca tta tcg atc ctg	192
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu	
50 55 60	
ctg att tat ctg ggc agt aca gga atg tgg ccg ctc cag tgg att ggc	240
Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly	
65 70 75 80	
gca ggt atg acg gcg tat gga tta ctc tat ttt atg gtg cac gac ggg	288
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly	
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ctg gtg cat caa cgt tgg cca ttc cgc tat att cca cgc aag ggc tac	336
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr	
100 105 110	
ctc aaa cgg ttg tat atg gcg cac cgt atg cat cac gcc gtc agg ggc	384
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly	
115 120 125	
aaa gaa ggt tgt gtt tct ttt ggc ttc ctc tat gcg ccg ccc ctg tca	432
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser	
130 135 140	
aaa ctt cag gcg acg ctc cgg gaa aga cat ggc gct aga gcg ggc gct	480
Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala	
145 150 155 160	
gcc aga gat gcg cag ggc ggg gag gat gag ccc gca tcc ggg aag taa	528
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<210> 34  
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 <212> PRT  
 <213> Erwinia uredovora

<400> 34

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Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp  
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Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe  
 35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu

50

55

60

Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly  
 65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly  
 85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr  
 100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly  
 115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser  
 130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala  
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Ala Arg Asp Ala Gln Gly Glu Asp Glu Pro Ala Ser Gly Lys  
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 360  
 420  
 480

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gagtgacacc taaggaacta aatgccattc atttgtttta aaacgacatc aaagattgat	660
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 <211> 528  
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 <213> *Erwinia uredovora*

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 <212> DNA  
 <213> *Nostoc sp. PCC73102*

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 <211> 617  
 <212> DNA  
 <213> Haematococcus pluvialis

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 <212> DNA  
 <213> Blakeslea trispora

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 <222> (4263)..(4263)  
 <223> n is a, c, g, or t

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 <212> DNA  
 <213> Blakeslea trispora

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